re-run

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/663,377_
Source: _1Fwo_
Date Processed by STIC: _9/25/03_

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IFWO

RAW SEQUENCE LISTING   DATE: 05/31/2005
PATENT APPLICATION: **US/10/663,377** TIME: 11:11:20

  Input Set : **N:\AMC\US10663377.raw**
  Output Set: **N:\CRF4\05312005\J663377.raw**

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 1 <110> APPLICANT: Liang, Yanbin
 2        Woodward, David F.
 3 <120> TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED
 4        VARIANTS AND METHODS OF USING SAME
 5 <130> FILE REFERENCE: 66872-028 (AR5746)
 6 <140> CURRENT APPLICATION NUMBER: US/10/663,377
 7 <141> CURRENT FILING DATE: 2003-09-15
 8 <160> NUMBER OF SEQ ID NOS: 38
 9 <170> SOFTWARE: FastSEQ for Windows Version 4.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 2022
13 <212> TYPE: DNA
14 <213> ORGANISM: Homo sapiens
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (298)...(2022)
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20        gtcctgctcg cggacccagg ggcgcccacg ccaggggcct ctttgggagg aagccgcagg 120
21        caccaaggga aatgagttcc ctttctccag cctctaaccg tctgggaacc atcctgatt 180
22        cccattgcca gtggagaagg tctcccctgg tgaagacttc gggagaacat gggagatgga 240
23        aatacattta ggagccggga tgcttcatct ggggtttaag agatccccat tgagcaa atg 300
24                                                                          Met
25                                                                          1
26        agg aaa ccg agg ctc atg aat ccc tgt tgt tac tat cca tgc cag cac   348
27        Arg Lys Pro Arg Leu Met Asn Pro Cys Cys Tyr Tyr Pro Cys Gln His
28                    5                   10                  15
29        cag ggc atc tgt gtc cgc ttc ggc ctt gac cgc tac cag tgt gac tgc   396
30        Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr Gln Cys Asp Cys
31                    20                  25                  30
32        acc cgc acg ggc tat tcc ggc ccc aac tgc acc atc cct ggc ctg tgg   444
33        Thr Arg Thr Gly Tyr Ser Gly Pro Asn Cys Thr Ile Pro Gly Leu Trp
34                    35                  40                  45
35        acc tgg ctc cgg aat tca ctg cgg ccc agc ccc tct ttc acc cac ttc   492
36        Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser Phe Thr His Phe
37         50                  55                  60                  65
38        ctg ctc act cac ggg cgc tgg ttc tgg gag ttt gtc aat gcc acc ttc   540
39        Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val Asn Ala Thr Phe
40                    70                  75                  80
41        atc cga gag atg ctc atg cgc ctg gta ctc aca gtg cgc tcc aac ctt   588
42        Ile Arg Glu Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn Leu
43                    85                  90                  95
44        atc ccc agt ccc ccc acc tac aac tca gca cat gac tac atc agc tgg   636
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45      Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp
46              100                 105                 110
47      gag tct ttc tcc aac gtg agc tat tac act cgt att ctg ccc tct gtg    684
48      Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val
49              115                 120                 125
50      cct aaa gat tgc ccc aca cgc atg gga acc aaa ggg aag aag cag ttg    732
51      Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln Leu
52      130                 135                 140                 145
53      cca gat gcc cag ctc ctg gcc cgc cgc ttc ctg ctc agg agg aag ttc    780
54      Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe
55                      150                 155                 160
56      ata cct gac ccc caa ggc acc aac ctc atg ttt gcc ttc ttt gca caa    828
57      Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala Gln
58                      165                 170                 175
59      cac ttc acc cac cag ttc ttc aaa act tct ggc aag atg ggt cct ggc    876
60      His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro Gly
61                      180                 185                 190
62      ttc acc aag gcc ttg ggc cat ggg gta gac ctc ggc cac att tat gga    924
63      Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr Gly
64              195                 200                 205
65      gac aat ctg gag cgt cag tat caa ctg cgg ctc ttt aag gat ggg aaa    972
66      Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys
67      210                 215                 220                 225
68      ctc aag tac cag gtg ctg gat gga gaa atg tac ccg ccc tcg gta gaa   1020
69      Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val Glu
70                      230                 235                 240
71      gag gcg cct gtg ttg atg cac tac ccc cga ggc atc ccg ccc cag agc   1068
72      Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln Ser
73                      245                 250                 255
74      cag atg gct gtg ggc cag gag gtg ttt ggg ctg ctt cct ggg ctc atg   1116
75      Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu Met
76                      260                 265                 270
77      ctg tat gcc acg ctc tgg cta cgt gag cac aac cgt gtg tgt gac ctg   1164
78      Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp Leu
79              275                 280                 285
80      ctg aag gct gag cac ccc acc tgg ggc gat gag cag ctt ttc cag acg   1212
81      Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr
82      290                 295                 300                 305
83      acc cgc ctc atc ctc ata ggg gag acc atc aag att gtc atc gag gag   1260
84      Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Glu
85                      310                 315                 320
86      tac gtg cag cag ctg agt ggc tat ttc ctg cag ctg aaa ttt gac cca   1308
87      Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro
88                      325                 330                 335
89      gag ctg ctg ttc ggt gtc cag ttc caa tac cgc aac cgc att gcc atg   1356
90      Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met
91                      340                 345                 350
92      gag ttc aac cat ctc tac cac tgg cac ccc ctc atg cct gac tcc ttc   1404
93      Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser Phe
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Input Set : **N:\AMC\US10663377.raw**
Output Set: **N:\CRF4\05312005\J663377.raw**

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94         355                 360                 365
95     aag gtg ggc tcc cag gag tac agc tac gag cag ttc ttg ttc aac acc   1452
96     Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr
97     370                 375                 380                 385
98     tcc atg ttg gtg gac tat ggg gtt gag gcc ctg gtg gat gcc ttc tct   1500
99     Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe Ser
100                        390                 395                 400
101      cgc cag att gct ggc cgg atc ggt ggg ggc agg aac atg gac cac cac   1548
102      Arg Gln Ile Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp His His
103                    405                 410                 415
104      atc ctg cat gtg gct gtg gat gtc atc agg gag tct cgg gag atg cgg   1596
105      Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg   ;
106              420                 425                 430
107      ctg cag ccc ttc aat gag tac cgc aag agg ttt ggc atg aaa ccc tac   1644
108      Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr
109          435                 440                 445
110      acc tcc ttc cag gag ctc gta gga gag aag gag atg gca gca gag ttg   1692
111      Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu
112      450                 455                 460                 465
113      gag gaa ttg tat gga gac att gat gcg ttg gag ttc tac cct gga ctg   1740·
114      Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu
115                        470                 475                 480
116      ctt ctt gaa aag tgc cat cca aac tct atc ttt ggg gag agt atg ata   1788
117      Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile
118                    485                 490                 495
119      gag att ggg gct ccc ttt tcc ctc aag ggt ctc cta ggg aat ccc atc   1836
120      Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile
121              500                 505                 510
122      tgt tct ccg gag tac tgg aag ccg agc aca ttt ggc ggc gag gtg ggc   1884
123      Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly
124          515                 520                 525
125      ttt aac att gtc aag acg gcc aca ctg aag aag ctg gtc tgc ctc aac   1932
126      Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn
127      530                 535                 540                 545
128      acc aag acc tgt ccc tac gtt tcc ttc cgt gtg ccg gat gcc agt cag   1980
129      Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln
130                    550                 555                 560
131      gat gat ggg cct gct gtg gag cga cca tcc aca gag ctc tga           2022
132      Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu Leu   *
133                    565                 570
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 574
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 2
140      Met Arg Lys Pro Arg Leu Met Asn Pro Cys Cys Tyr Tyr Pro Cys Gln
141      1                   5                   10                  15
142      His Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr Gln Cys Asp
143                    20                  25                  30
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144    Cys Thr Arg Thr Gly Tyr Ser Gly Pro Asn Cys Thr Ile Pro Gly Leu
145        35              40              45
146    Trp Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser Phe Thr His
147        50              55              60
148    Phe Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val Asn Ala Thr
149    65              70              75              80
150    Phe Ile Arg Glu Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn
151                85              90              95
152    Leu Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser
153                100             105             110
154    Trp Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser
155        115             120             125
156    Val Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln
157        130             135             140
158    Leu Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys
159    145             150             155             160
160    Phe Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala
161                165             170             175
162    Gln His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro
163                180             185             190
164    Gly Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr
165        195             200         '       205
166    Gly Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly
167        210             215             220
168    Lys Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val
169    225             230             235             240
170    Glu Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln
171            .       245             250             255
172    Ser Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu
173            .       260             .   265             270
174    Met Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp
175        275             280             285
176    Leu Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln
177        290             295             300
178    Thr Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu
179    305             310             315             320
180    Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp
181                325             330             335
182    Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala
183                340             345             350
184    Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser
185                355             360             365
186    Phe Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn
187        370             375             380
188    Thr Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe
189    385             390             395             400
190    Ser Arg Gln Ile Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp His
191                405             410             415
192    His Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met
```

```
193                     420                 425                 430
194      Arg Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro
195              435                 440                 445
196      Tyr Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu
197          450                 455                 460
198      Leu Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly
199      465                 470                 475                 480
200      Leu Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met
201              485                 490                 495
202      Ile Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro
203              500                 505                 510
204      Ile Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val
205          515                 520                 525
206      Gly Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu
207          530                 535                 540
208      Asn Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser
209      545                 550                 555                 560
210      Gln Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu Leu
211              565                 570
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 1818
215 <212> TYPE: DNA
216 <213> ORGANISM: Homo sapiens
217 <220> FEATURE:
218 <221> NAME/KEY: CDS
219 <222> LOCATION: (298)...(1620)
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223      caccaaggga aatgagttcc ctttctccag cctctaaccg tctgggaacc catcctgatt 180
224      cccattgcca gtggagaagg tctcccctgg tgaagacttc gggagaacat gggagatgga 240
225      aatacattta ggagccggga tgcttcatct ggggtttaag agatccccat tgagcaa atg 300
226                                                                      Met
227                                                                      1
228      agg aaa ccg agg ctc agg aag aag cag ttg cca gat gcc cag ctc ctg  348
229      Arg Lys Pro Arg Leu Arg Lys Lys Gln Leu Pro Asp Ala Gln Leu Leu
230              5                   10                  15
231      gcc cgc cgc ttc ctg ctc agg agg aag ttc ata cct gac ccc caa ggc  396
232      Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp Pro Gln Gly
233              20                  25                  30
234      acc aac ctc atg ttt gcc ttc ttt gca caa cac ttc acc cac cag ttc  444
235      Thr Asn Leu Met Phe Ala Phe Phe Ala Gln His Phe Thr His Gln Phe
236          35                  40                  45
237      ttc aaa act tct ggc aag atg ggt cct ggc ttc acc aag gcc ttg ggc  492
238      Phe Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys Ala Leu Gly
239      50                  55                  60                  65
240      cat ggg gta gac ctc ggc cac att tat gga gac aat ctg gag cgt cag  540
241      His Gly Val Asp Leu Gly His Ile Tyr Gly Asp Asn Leu Glu Arg Gln
242              70                  75                  80
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VERIFICATION SUMMARY DATE: 05/31/2005
PATENT APPLICATION: **US/10/663,377** TIME: 11:11:21

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